AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1 - 5.   (Canceled)

6.   (Currently amended)   The method of claim 8, wherein the DNA methylation pattern for the test ~~stem~~-cell, test ~~stem cell~~-tissue, or test ~~stem cell~~-nucleus and the differentiation state-specific DNA methylation pattern each comprise information on the methylation state of at least about 1,000 gene regions.

7.   (Canceled)

8.   (Currently amended)   A method of identifying the differentiation state of a test ~~stem~~-cell, test ~~stem cell~~-tissue, or test ~~stem cell~~-nucleus, wherein the test cell, test tissue, or test nucleus is selected from a stem cell, a stem cell tissue, a stem cell nucleus, a differentiating stem cell, a differentiating stem cell tissue, a differentiating stem cell nucleus, a cell differentiated from a stem cell, a tissue differentiated from a stem cell tissue, and a nucleus differentiated from a stem cell nucleus comprising:

obtaining a DNA methylation pattern for the test ~~stem~~-cell, test ~~stem cell~~-tissue, or test ~~stem cell~~-nucleus, wherein the DNA methylation pattern for the test ~~stem~~-cell, test ~~stem cell~~-tissue, or test ~~stem cell~~-nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a differentiation state-specific DNA methylation pattern for one or more ~~stem~~-cell, ~~stem cell~~-tissue, or ~~stem cell~~-nucleus of known differentiation state, wherein the one or more cell, tissue, or nucleus of known differentiation state is selected from a stem cell, a stem cell tissue, a stem cell nucleus, a differentiating stem cell, a differentiating stem cell tissue, a differentiating stem cell nucleus, a cell differentiated from a stem cell, a tissue differentiated from a stem cell tissue, and a nucleus differentiated from a stem cell nucleus; and,

comparing the DNA methylation pattern for the test ~~stem~~ cell, test ~~stem cell~~ tissue, or test ~~stem cell~~ nucleus with the differentiation state-specific DNA methylation pattern,

wherein the differentiation state of the test ~~stem~~ cell, test ~~stem cell~~ tissue, or test ~~stem cell~~ nucleus is identified if the DNA methylation pattern of the test ~~stem~~ cell, test ~~stem cell~~ tissue, or test ~~stem cell~~ nucleus matches the differentiation state-specific DNA methylation pattern.

9.   (Previously presented)   The method of claim 8, wherein the DNA methylation patterns are obtained by generating RLGS profiles.

10 - 18.   (Canceled)

19.   (Currently amended) The method of claim 8, wherein the test ~~stem~~ cell, test ~~stem cell~~ tissue, or test ~~stem cell~~ nucleus is an embryonic stem cell, embryonic stem cell tissue, ~~or~~ embryonic stem cell nucleus, differentiating embryonic stem cell, differentiating embryonic stem cell tissue, differentiating embryonic stem cell nucleus, a cell differentiated from an embyronic stem cell, a tissue differentiated from an embryonic stem cell tissue, or a nucleus differentiated from an embryonic stem cell nucleus.

20.   (Currently amended) The method of claim 8, wherein the differentiation state of the one or more ~~stem~~ cell, ~~stem cell~~ tissue, or ~~stem cell~~ nucleus of known differentiation state is differentiated.

21.   (Currently amended) The method of claim 8, wherein the differentiation state of the one or more ~~stem~~ cell, ~~stem cell~~ tissue, or ~~stem cell~~ nucleus of known differentiation state is undifferentiated.

22.   (Currently amended) A method of identifying a test ~~stem~~ cell, test ~~stem cell~~ tissue, or test ~~stem cell~~ nucleus, wherein the test cell, test tissue, or test nucleus is selected from a stem cell, a stem cell tissue, a stem cell nucleus, a differentiating stem cell, a differentiating stem cell tissue, a differentiating stem

cell nucleus, a cell differentiated from a stem cell, a tissue differentiated from a
stem cell tissue, and a nucleus differentiated from a stem cell nucleus, comprising:

obtaining a DNA methylation pattern for the test ~~stem~~ cell,
test ~~stem cell~~ tissue, or test ~~stem cell~~ nucleus, wherein the
DNA methylation pattern for the test ~~stem~~ cell, test ~~stem~~
~~cell~~ tissue, or test ~~stem cell~~ nucleus comprises information
on the methylation state of CpG at a plurality of gene
regions;

obtaining a cell-, tissue-, or nucleus-specific DNA
methylation pattern for one or more known types of ~~stem~~
cell, ~~stem cell~~ tissue, or ~~stem cell~~ nucleus; wherein the one
or more known types of ~~stem~~ cell, ~~stem cell~~ tissue, or ~~stem~~
~~cell~~ nucleus is selected from undifferentiated embryonic
stem cell, ~~differentiated~~ differentiating embryonic stem
cell, cell differentiated from embryonic stem cell,
undifferentiated trophoblast stem cell, ~~and differentiated~~
differentiating trophoblast stem cell, and cell differentiated
from trophoblast stem cell; and,

comparing the DNA methylation pattern for the test ~~stem~~
cell, test ~~stem cell~~ tissue, or test ~~stem cell~~ nucleus with the
cell-, tissue-, or nucleus-specific DNA methylation pattern
of the known ~~stem~~ cell, ~~stem cell~~ tissue, or ~~stem cell~~
nucleus to permit identification of the test ~~stem~~ cell, test
~~stem cell~~ tissue, or test ~~stem cell~~ nucleus as one of the
known types of ~~stem~~ cell, ~~stem cell~~ tissue, or ~~stem cell~~
nucleus;

wherein a match to the cell-, tissue-, or
nucleus-specific DNA methylation pattern of the
undifferentiated embryonic stem cell identifies the

test stem cell, test stem-cell-tissue, or test stem cell nucleus as undifferentiated embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the differentiated differentiating embryonic stem cell identifies the test stem cell, test stem-cell tissue, or test stem-cell-nucleus as differentiated differentiating embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the cell differentiated from embryonic stem cell identifies the test cell, test tissue, or test nucleus as differentiated from embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the undifferentiated trophoblast stem cell identifies the test stem cell, test stem-cell tissue, or test stem cell nucleus as undifferentiated trophoblast stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the differentiated differentiating trophoblast stem cell identifies the test stem cell, test stem-cell tissue, or test stem-cell-nucleus as differentiated differentiating trophoblast stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the cell differentiated from trophoblast stem cell identifies the test cell, test tissue, or test nucleus as differentiated from trophoblast stem cell.

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23.   (Previously presented)   The method of claim 22, wherein the DNA methylation

patterns are obtained by generating RLGS profiles.

24.   (New) The method of claim 8, wherein the differentiation state of the one

or more cell, tissue, or nucleus of known differentiation state is differentiating.